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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/835,107A

DATE: 03/20/2003

TIME: 16:05:40

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\03202003\I835107A.raw

3 <110> APPLICANT: University of British Columbia, et al.  
 5 <120> TITLE OF INVENTION: CXCR4 AGONIST TREATMENT OF HEMATOPOIETIC CELLS  
 7 <130> FILE REFERENCE: 80021-255  
 9 <140> CURRENT APPLICATION NUMBER: US 09/835,107A  
 10 <141> CURRENT FILING DATE: 2001-04-12  
 12 <150> PRIOR APPLICATION NUMBER: CA 2,305,036  
 13 <151> PRIOR FILING DATE: 2000-04-12  
 15 <150> PRIOR APPLICATION NUMBER: US 60/232,425  
 16 <151> PRIOR FILING DATE: 2000-09-14  
 18 <150> PRIOR APPLICATION NUMBER: CA 2,335,109  
 19 <151> PRIOR FILING DATE: 2001-02-23  
 21 <160> NUMBER OF SEQ ID NOS: 31  
 23 <170> SOFTWARE: PatentIn Ver. 2.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 67  
 27 <212> TYPE: PRT  
 28 <213> ORGANISM: Homo sapiens  
 30 <220> FEATURE:  
 31 <223> OTHER INFORMATION: SDF-1 alpha  
 33 <220> FEATURE:  
 34 <221> NAME/KEY: MISC\_FEATURE  
 35 <222> LOCATION: (1)..(67)  
 36 <223> OTHER INFORMATION: A pegylation moiety may be provided at any position on the  
 37 sequence.  
 39 <400> SEQUENCE: 1  
 40 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser  
 41 1 5 10 15  
 43 His Val Ala Arg Ala Asn Val Lys His Leu Lys Ile Leu Asn Thr Pro  
 44 20 25 30  
 46 Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys Asn Asn Asn Arg Gln  
 47 35 40 45  
 49 Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys  
 50 50 55 60  
 52 Ala Leu Asn  
 53 65  
 56 <210> SEQ ID NO: 2  
 57 <211> LENGTH: 93  
 58 <212> TYPE: PRT  
 59 <213> ORGANISM: Homo sapiens  
 61 <220> FEATURE:  
 62 <223> OTHER INFORMATION: SDF-1 Precursor, PBSF  
 64 <220> FEATURE:  
 65 <221> NAME/KEY: MISC\_FEATURE

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66 <222> LOCATION: (1)..(93)  
 67 <223> OTHER INFORMATION: A pegylation moiety may be provided at any position on the  
 68 sequence.  
 70 <400> SEQUENCE: 2  
 71 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
 72 1 5 10 15  
 74 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
 75 20 25 30  
 77 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
 78 35 40 45  
 80 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
 81 50 55 60  
 83 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
 84 65 70 75 80  
 86 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
 87 85 90  
 90 <210> SEQ ID NO: 3  
 91 <211> LENGTH: 93  
 92 <212> TYPE: PRT  
 93 <213> ORGANISM: Homo sapiens  
 95 <220> FEATURE:  
 96 <223> OTHER INFORMATION: SDF-1 beta  
 98 <220> FEATURE:  
 99 <221> NAME/KEY: MISC FEATURE  
 100 <222> LOCATION: (1)..(93)  
 101 <223> OTHER INFORMATION: A pegylation moiety may be provided at any position on the  
 102 sequence.  
 104 <400> SEQUENCE: 3  
 105 Met Asn Ala Lys Val Val Val Val Leu Val Leu Val Leu Thr Ala Leu  
 106 1 5 10 15  
 108 Cys Leu Ser Asp Gly Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys  
 109 20 25 30  
 111 Arg Phe Phe Glu Ser His Val Ala Arg Ala Asn Val Lys His Leu Lys  
 112 35 40 45  
 114 Ile Leu Asn Thr Pro Asn Cys Ala Leu Gln Ile Val Ala Arg Leu Lys  
 115 50 55 60  
 117 Asn Asn Asn Arg Gln Val Cys Ile Asp Pro Lys Leu Lys Trp Ile Gln  
 118 65 70 75 80  
 120 Glu Tyr Leu Glu Lys Ala Leu Asn Lys Arg Phe Lys Met  
 121 85 90  
 124 <210> SEQ ID NO: 4  
 125 <211> LENGTH: 17  
 126 <212> TYPE: PRT  
 127 <213> ORGANISM: Artificial Sequence  
 129 <220> FEATURE:  
 130 <223> OTHER INFORMATION: Synthesised in Laboratory: SDF-1(1-17): or  
 131 CTCE9902  
 133 <400> SEQUENCE: 4  
 134 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Glu Ser

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135      1                      5                      10                      15
137 His
141 <210> SEQ ID NO: 5
142 <211> LENGTH: 6
143 <212> TYPE: PRT
144 <213> ORGANISM: Artificial Sequence
146 <220> FEATURE:
147 <223> OTHER INFORMATION: Synthesised in Laboratory
149 <400> SEQUENCE: 5
150 Arg Phe Phe Glu Ser His
151      1                      5
154 <210> SEQ ID NO: 6
155 <211> LENGTH: 9
156 <212> TYPE: PRT
157 <213> ORGANISM: Artificial Sequence
159 <220> FEATURE:
160 <223> OTHER INFORMATION: Synthesised in Laboratory
162 <400> SEQUENCE: 6
163 Lys Pro Val Ser Leu Ser Tyr Arg Cys
164      1                      5
167 <210> SEQ ID NO: 7
168 <211> LENGTH: 9
169 <212> TYPE: PRT
170 <213> ORGANISM: Artificial Sequence
172 <220> FEATURE:
173 <221> NAME/KEY: DISULFID
174 <222> LOCATION: (9)
175 <223> OTHER INFORMATION: Disulphide linkage may form between two cys
176     residues at position 9 of each of two monomers
177     thereby forming a dimer.
179 <220> FEATURE:
180 <223> OTHER INFORMATION: Synthesised in Laboratory:
181     SDF-1(1-9)2-C9/C9-cysteine dimer: or CTCE9901
183 <400> SEQUENCE: 7
184 Lys Pro Val Ser Leu Ser Tyr Arg Cys
185      1                      5
188 <210> SEQ ID NO: 8
189 <211> LENGTH: 9
190 <212> TYPE: PRT
191 <213> ORGANISM: Artificial Sequence
193 <220> FEATURE:
194 <223> OTHER INFORMATION: Synthesised in Laboratory
196 <220> FEATURE:
197 <221> NAME/KEY: BINDING
198 <222> LOCATION: (9)
199 <223> OTHER INFORMATION: Linking Moiety (may be lysine with both the alpha and the
200     epsilon amino groups of the lysine being associated with
201     the covalent (amide) bond formation) may bind here allowing
202     formation of a dimer.

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204 <400> SEQUENCE: 8  
 205 Lys Pro Val Ser Leu Ser Tyr Arg Cys  
 206 1 5  
 209 <210> SEQ ID NO: 9  
 210 <211> LENGTH: 8  
 211 <212> TYPE: PRT  
 212 <213> ORGANISM: Artificial Sequence  
 214 <220> FEATURE:  
 215 <223> OTHER INFORMATION: Synthesised in Laboratory  
 217 <220> FEATURE:  
 218 <221> NAME/KEY: BINDING  
 219 <222> LOCATION: (8)  
 220 <223> OTHER INFORMATION: Linking Moiety (may be lysine with both the alpha and the  
 221 epsilon amino groups of the lysine being associated with  
 222 the covalent (amide) bond formation) may bind here allowing  
 223 formation of a dimer.  
 225 <400> SEQUENCE: 9  
 226 Lys Pro Val Ser Leu Ser Tyr Arg  
 227 1 5  
 230 <210> SEQ ID NO: 10  
 231 <211> LENGTH: 30  
 232 <212> TYPE: PRT  
 233 <213> ORGANISM: Artificial Sequence  
 235 <220> FEATURE:  
 236 <221> NAME/KEY: DOMAIN  
 237 <222> LOCATION: (15)..(17)  
 238 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
 239 G's) may be used in variable numbers, such as 2, 3  
 240 or 4 glycines.  
 242 <220> FEATURE:  
 243 <223> OTHER INFORMATION: Synthesised in Laboratory:  
 244 SDF-1(1-14)-(G)3-SDF-1(55-67) acid  
 246 <400> SEQUENCE: 10  
 247 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly  
 248 1 5 10 15  
 250 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn  
 251 20 25 30  
 254 <210> SEQ ID NO: 11  
 255 <211> LENGTH: 31  
 256 <212> TYPE: PRT  
 257 <213> ORGANISM: Artificial Sequence  
 259 <220> FEATURE:  
 260 <221> NAME/KEY: DOMAIN  
 261 <222> LOCATION: (16)..(19)  
 262 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
 263 G's) may be used in variable numbers, such as 2, 3  
 264 or 4 glycines.  
 266 <220> FEATURE:  
 267 <223> OTHER INFORMATION: Synthesised in Laboratory:

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268 SDF-1(1-14)-(G)4-SDF-1(55-67) acid: or CTCE0013  
 270 <400> SEQUENCE: 11  
 271 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly  
 272 1 5 10 15  
 274 Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn  
 275 20 25 30  
 278 <210> SEQ ID NO: 12  
 279 <211> LENGTH: 30  
 280 <212> TYPE: PRT  
 281 <213> ORGANISM: Artificial Sequence  
 283 <220> FEATURE:  
 284 <221> NAME/KEY: DOMAIN  
 285 <222> LOCATION: (15)..(17)  
 286 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
 287 G's) may be used in variable numbers, such as 2, 3  
 288 or 4 glycines.  
 290 <220> FEATURE:  
 291 <223> OTHER INFORMATION: Synthesised in Laboratory:  
 292 SDF-1(1-14)-(G)3-SDF-1(55-67) amide  
 294 <220> FEATURE:  
 295 <221> NAME/KEY: MOD\_RES  
 296 <222> LOCATION: (30)  
 297 <223> OTHER INFORMATION: AMIDATION  
 299 <400> SEQUENCE: 12  
 300 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly  
 301 1 5 10 15  
 303 Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn  
 304 20 25 30  
 307 <210> SEQ ID NO: 13  
 308 <211> LENGTH: 31  
 309 <212> TYPE: PRT  
 310 <213> ORGANISM: Artificial Sequence  
 312 <220> FEATURE:  
 313 <221> NAME/KEY: DOMAIN  
 314 <222> LOCATION: (15)..(18)  
 315 <223> OTHER INFORMATION: spacer monomers (such as the illustrated glycine  
 316 G's) may be used in variable numbers, such as 2, 3  
 317 or 4 glycines.  
 319 <220> FEATURE:  
 320 <223> OTHER INFORMATION: Synthesised in Laboratory:  
 321 SDF-1(1-14)-(G)4-SDF-1(55-67) amide: or CTCE0017  
 323 <220> FEATURE:  
 324 <221> NAME/KEY: MOD\_RES  
 325 <222> LOCATION: (31)  
 326 <223> OTHER INFORMATION: AMIDATION  
 328 <400> SEQUENCE: 13  
 329 Lys Pro Val Ser Leu Ser Tyr Arg Cys Pro Cys Arg Phe Phe Gly Gly  
 330 1 5 10 15  
 332 Gly Gly Leu Lys Trp Ile Gln Glu Tyr Leu Glu Lys Ala Leu Asn

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/835,107A

DATE: 03/20/2003

TIME: 16:05:41

Input Set : A:\seqlist.txt

Output Set: N:\CRF4\03202003\I835107A.raw